



Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy Boo

Search for Limits Preview/Index History Clipboard Details
 Show: ☐ 1: [AW136973](#). UI-H-BI1-acu-a-01...[gi:6141106][Links](#)**IDENTIFIERS**

dbEST Id: 3289020
EST name: UI-H-BI1-acu-a-01-0-UI.s1
GenBank Acc: AW136973
GenBank gi: 6141106

CLONE INFO

Clone Id: IMAGE:2715528 (3')
Source: NCI
DNA type: cDNA

PRIMERS

Sequencing: M13 Forward
PolyA Tail: yes

SEQUENCE

```
TTTTTTTTTTTTTTTTTCTTAAATAGTCACCAGACGGCTTTAACAAGGAAAGCTCTTCT  
GATCTTCTAATATTGAGGATTTTGCAGATATCACTGACAGCTTTAAAAACACAGCTGAG  
AAGCTGACTCGCAACCTCACCATCTTCAAATTCGGCAGACGAAGGCGCAGCATTATATGC  
TGAGGGGTGAAGAGAAGCTTTGCATCTGCCTGGACCCC
```

Entry Created: Oct 29 1999
Last Updated: Oct 29 1999

COMMENTS

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares
Lab Clone distribution: NCI-CGAP clone distribution
information can be found through the I.M.A.G.E.
Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

LIBRARY

Lib Name: NCI_CGAP_Sub3
Organism: Homo sapiens
Tag Seq: AAGTG
Tag Tissue: prostate
Tag Lib: NCI_CGAP_Pr22
Lab host: DH10B (Life Technologies)
Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker
R. Site 1: Not I
R. Site 2: Eco RI
Description: The NCI_CGAP_Sub3 library is a subtracted library derived from the NCI_CGAP_Sub1 library, which is a subtracted library derived from BI. BI constitutes a mixture of 21

normalized or subtracted NCI_CGAP libraries: NCI_CGAP_Co4, NCI_CGAP_Pr22, NCI_CGAP_Pr28, NCI_CGAP_Co10, NCI_CGAP_Co16, NCI_CGAP_Kid5, NCI_CGAP_Kid12, NCI_CGAP_Kid3, NCI_CGAP_Kid11, NCI_CGAP_Lym2, NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_CLL1, NCI_CGAP_Lei2, NCI_CGAP_Brn23, NCI_CGAP_Lu5, NCI_CGAP_Lu24, NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6, NCI_CGAP_Brn25. These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below: NCI_CGAP_Kid3 pool 1 LLAM 3334-3337, 3682-3683, 3798-3803 (IMAGE CloneIDs 1322376-1323911, 1456008-1456775, 1500552-1502855); NCI_CGAP_Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE CloneIDs 1323912-1325831, 1471368-1472903, 1492104-1493255); NCI_CGAP_Lu5 pool 1 LLAM 3575-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991, 1520904-1522439); NCI_CGAP_GC4 pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631, 1469064-1470983, 1475592-1476743); NCI_CGAP_Pr22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs 985608-986759, 1101192-1101959, 1217928-1220615); NCI_CGAP_Co10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE CloneIDs 1057416-1061255, 1144584-1145351). Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.

SUBMITTER

Name: Robert Strausberg, Ph.D.
E-mail: cgapbs-r@mail.nih.gov

CITATIONS

Title: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Authors: NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
Year: 1997
Status: Unpublished

MAP DATA

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Dec 1 2003 12:53:28